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RAW SEQUENCE LISTING

DATE: 08/09/2002

PATENT APPLICATION: US/10/086,542A

TIME: 15:49:57

Input Set : N:\Crf3\RULE60\10086542A.RAW Output Set: N:\CRF4\08092002\J086542A.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
            (i) APPLICANT: Wahl, Geoffrey M
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                            O'Gorman, Stephen V
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           (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
     8
                                     MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
     9
                                     THEREFOR
    10
           (iii) NUMBER OF SEQUENCES: 4
    12
            (iv) CORRESPONDENCE ADDRESS:
    14
                  (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
    15
                  (B) STREET: 444 South Flower Street, Suite 2000
    16
                  (C) CITY: Los Angeles
    17
                  (D) STATE: California
    18
                                                              ENTERED
                  (E) COUNTRY: USA
    19
                  (F) ZIP: 90071
    20
             (V) COMPUTER READABLE FORM:
    22
                  (A) MEDIUM TYPE: Floppy disk
    23
                  (B) COMPUTER: IBM PC compatible
     24
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     25
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     26
            (vi) CURRENT APPLICATION DATA:
     28
                  (A) APPLICATION NUMBER: US/10/086,542A
C-->29
                  (B) FILING DATE: 28-Feb-2002
C--> 30
                  (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: US/08/484,324
     35
                  (B) FILING DATE: 07-JUN-1995
     36
          (viii) ATTORNEY/AGENT INFORMATION:
     39
                  (A) NAME: Reiter, Stephen E
     40
                  (B) REGISTRATION NUMBER: 31,192
     41
                  (C) REFERENCE/DOCKET NUMBER: P41 9984
     42
            (ix) TELECOMMUNICATION INFORMATION:
     44
                  (A) TELEPHONE: (619) 546-4737
     45
                  (B) TELEFAX: (619) 546-9392
     46
        (2) INFORMATION FOR SEQ ID NO: 1:
     49
             (i) SEQUENCE CHARACTERISTICS:
     51
                   (A) LENGTH: 1380 base pairs
     52
                   (B) TYPE: nucleic acid
     53
                   (C) STRANDEDNESS: single
                   (D) TOPOLOGY: linear
     55
            (ii) MOLECULE TYPE: DNA (genomic)
     57
            (vii) IMMEDIATE SOURCE:
     60
                   (B) CLONE: NATIVE FLP
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PATENT APPLICATION: US/10/086,542A

DATE: 08/09/2002 TIME: 15:49:58

68 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 68 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 67 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 67 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 67 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 67 ATG CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 67 ATG GIN Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 67 20 25 30 68 TTA TGT GCT GAA CAC TATA TTA TGT TGT TGG ATG ATA ACA CAT AAC 69 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 60 35 40 61 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 61 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gin Phe Lys 63 GAG ACA GCA AAA GCA ACA ATT CTG GAA GCC TCA GTT AAA ACA 65 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gin Phe Lys 65 07 75 80 60 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAA AAA TTC 65 TS	63		(ix)				KEY	· Cl	ns												
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 70 ATG CCA CAT ATG ATA TATA TCTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 71 Met Pro Gln Phe Asp IIe Leu Cys Lys Thr Pro Pro Lys Val Leu Val 72 1 5 15 74 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCA CCT AGG GTG GAA AATA GCA 75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys IIe Ala 76 20 25 30 8 TTA TGT GCT GCT GAA CCT AAC TAT TTA TGT TGG ATG ATT ACA CAT AAC 79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 80 35 40 40 82 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AATA ACT ATC ATA 83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr IIe Ile 84 50 55 86 AGC AAT TCG CTG GAT TTC GAT ATT GTC TATA ATA CTA CATA 87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys 88 65 70 80 80 75 80 60 81 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu 92 90 92 90 93 95 94 ATT CCT GCT TGG GAA TTT ACA ATT ATT ATT TTT TGT TGA GC CAA AAA CAT 95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His 100 105 105 100 105 105 100 105 105 100 105 101 105 104 105 105 106 AAA ATA CAG TTC GAA AAA CAT 480 480 480 480 480 480 480 480 480 480	64 65									69											
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102 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA AAT G CTT 103 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu 104 130 135 140 106 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480 107 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys 108 145 150 150 160 110 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528 111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr 112 165 170 170 114 TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC 115 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe 116 180 185 118 AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TCT TAAA TTA GTC CAA AAT 119 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn 120 195 200 122 AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG GCA AGG GGT AGG ATC GAT 126 ACC CTT ACT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT 120 215 220 121 AGC CTT ACT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT 120 215 220 121 AGC CTT ACT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT 120 215 220 121 AGC CTT ACT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT 120 215 220			Sei			E 111	т ъ.	5p .		120)					12	5				
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122 AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA 123 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr 124 210 220 126 ACC CTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT 720	1 1	20		1	95					20	0					20	,				672
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126 AGC GIT AGT AGG GAG ATT THE Phe Phe Ser Ala Arg Gly Arg Ile Asp 127 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp 240	1	27 S	er V	al S	Ser A	\rg	His	Ile	ту:	r Ph	e P	ne S	er	Ald	AL.	a er	.у А	. y 1	.10	IID _P	
128 225 230 235 240								230)					∠33	,					230	

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130 CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA	768
130 CCA CIT GIA IAI IIG GAI GIA PIL LEU Arg Asn Ser Glu Pro Val Leu 131 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu	Ł
132 245 250 253	
134 AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC	816
135 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr	•
136 260	864
138 CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG 139 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys	3
. 655	
142 AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCI	r 912
143 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser	<i>:</i>
144 290 295 300	
146 CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA	-
147 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu)
1/8 3/5	
150 ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT 151 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser	r
330 333	
152 325 154 GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAS	r 1056
155 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asj	ρ
156 340 345	
158 CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TC	A 1104
159 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro 11e Se.	r
160 355 360 365	
162 AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TG	-
163 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro İle Glu Glu Tr	۲
164 370 375 380 166 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TA	C 1200
166 CAG CAT ATA GAA CAG CIA AAG GGT AGT GGT GIN GIN SET ILE ATG TY 167 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Gly Ser Ile Arg Ty	r
167 GIN HIS THE GIR GIN LEW LIPS CITY DOLL HER 198 110 40	0
170 CCC GCA TGG ATT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TC	A 1248
171 Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Se	r
172 405 410 415	
174 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT	1299
175 Ser Tyr Ile Asn Arg Arg Ile	
176 420	TGA 1359
178 ATCCCGTTCT TCTCATGTAT ATATATATA AGGCAACACG CAGATATAGG TGCGACG	1380
180 ACAGTGAGCT GTATGTGCGC A 183 (2) INFORMATION FOR SEQ ID NO: 2:	
185 (i) SEQUENCE CHARACTERISTICS: 186 (A) LENGTH: 423 amino acids	
187 (B) TYPE: amino acid	
188 (D) TOPOLOGY: linear	
190 (ii) MOLECULE TYPE: protein	
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	. 1
194 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Va	s, ab.
195 1 5 10 15 197 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Al	La
7E 3U	
198 20 25	

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200 201	Leu	Cys	Ala 35	Ala	Glu	Leu	Thr	Tyr 40	Leu	Cys	Trp	Met	Ile 45	Thr	His	Asn
203	Gly	Thr 50		Ile	Lys	Arg	Ala 55	Thr	Phe	Met	Ser	Tyr 60	Asn	Thr	Ile	Ile
		Asn	Ser	Leu	Ser			Ile	Val	Asn	Lys 75	-	Leu	Gln	Phe	Lys 80
207 209	65 Tyr	Lys	Thr	Gln	Lys	70 Ala	Thr	Ile	Leu	Glu		Ser	Leu	Lys	Lys	
210	Tle	Pro	Δla	Trp	85 Glu	Phe	Thr	Ile	Ile	90 Pro	Tyr	Tyr	Gly	Gln	95 Lys	His
213				100					105					110		
216			115					120					125	Gln		
218 219	Ser	Ser 130	Glu	Glu	Ala	Asp	Lys 135	Gly	Asn	Ser	His	Ser 140	Lys	Lys	Met	Leu
221		Ala	Leu	Leu	ser			Glu	Ser	Ile	Trp 155	Glu	Ile	Thr	Glu	Lys 160
222	145	_	_	_	- 1	150	m	mb	Com	7~~		Thr	T.376	Thr	T.VS	-
225					165					170				Thr	175	
227 228	Leu	Tyr	Gln	Phe 180	Leu	Phe	Leu	Ala	Thr 185	Phe	Ile	Asn	Cys	Gly 190	Arg	Pne
230	Ser	Asp		Lys	Asn	Val	Asp	Pro 200	Lys	Ser	Phe	Lys	Leu 205	Val	Gln	Asn
231	_	m	195	61	37a 1	т1 о	T10		Cve	T.e.u	Val	Thr		Thr	Lvs	Thr
234		210					215					220	•			
237	225					230					235			Arg		240
239	Pro	Leu	Val	Tyr	Leu 245		Glu	Phe	Leu	Arg 250	Asn	Ser	Glu	Pro	Val 255	Leu
240	T ***	7 ~~	V-1	λen	Δrσ	Thr	Glv	Asn	Ser			Asn	Lys	Gln	Glu	Tyr
243				260					265					270		
246			275					280					285			Lys
248 249		Asn 290	Ala	Pro	Tyr	Ser	Ile 295		Ala	Ile	Lys	Asn 300	Ģly	Pro	Lys	Ser
251	His	Ile	Glv	Arq	His	Leu			Ser	Phe	Leu	Ser	Met	Lys	Gly	Leu
252	305					310					315					320
254	Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	Ser	Asp	Lys	Arg	Ala	Ser
255					325					330	1				335	
257	Ala	Val	Ala			Thr	Tyr	Thr			Ile	Thr	Ala	ILE	Pro	Asp
258				340)	_		_	345			m		350		Cor
		Tyr			Leu	Val	Ser			туг	. ATa	туг	365	PIO	ıre	Ser
261			355			.	.	360		. mh~	. Aan	Dro			Glu	Ψrn
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264		370	T1^		. Gla	T.211			, Ser	• Ala	Glu			· Ile	Arq	Tyr
	385		TTE	GIU	. 311	390		. J_y	501		395	5			,	400
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270					405					410)				415	5
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275	(2) INFORMATION FOR SEQ ID NO: 3:	
277	(i) SEQUENCE CHARACTERISTICS:	
278	(A) LENGTH: 34 base pairs	
279	(B) TYPE: nucleic acid	
280	(C) STRANDEDNESS: single	
281	(D) TOPOLOGY: linear	
283	(ii) MOLECULE TYPE: DNA (genomic)	
287	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
289	GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC	34
291	(2) INFORMATION FOR SEQ ID NO: 4:	
293	(i) SEQUENCE CHARACTERISTICS:	
294		
295	•	
296		
297	, ,	
299	(ii) MOLECULE TYPE: DNA (genomic)	
303	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
305	GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG	60
307	GAACTTCA	68

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VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]